SIR epidemics on random graphs with clustering\textsuperscript{a}

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\textsuperscript{a}This presentation is based on a master’s project under the supervision of Dr. Pieter Trapman.
Some questions of interest in epidemic modelling:

1. What is the impact of the underlying social network on the spread of the disease?
2. What is the probability of a large outbreak?
3. If a major outbreak occurs, how large will it be?
4. What control measures (e.g. vaccination) are necessary to contain the disease?
At each time point, individuals are divided into three groups according to health status:

- S - Susceptible
- I - Infectious
- R - Recovered
A social network can be represented by a directed graph:

- Nodes represent individuals
- Edges represent relationships
- Edge weights represent times of transmission
Reproduction numbers

- Basic reproduction number $R_0$
- Expected number of cases caused by a "typical" infected during the early phase
- Threshold properties: $R_0 \leq 1 \iff$ major outbreak not possible
  $R_0 > 1 \iff$ major outbreak might occur
- Preventive/control measures: For simple models, a fraction
  
  $$1 - \frac{1}{R_0}$$

  has to be vaccinated with a perfect vaccine to "surely" prevent a major outbreak
Estimated values of $R_0$ for the 2014 Ebola outbreak with 95% confidence intervals:

<table>
<thead>
<tr>
<th>Country</th>
<th>$R_0$ (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Guinea</td>
<td>1.51 (1.50-1.52)</td>
</tr>
<tr>
<td>Sierra Leone</td>
<td>2.53 (2.41-2.67)</td>
</tr>
<tr>
<td>Liberia</td>
<td>1.59 (1.57-1.60)</td>
</tr>
</tbody>
</table>
Multi-type Galton-Watson processes

- \( s \in \mathbb{N} \) types of individuals
- Individuals reproduce independently at age 1, offspring distribution determined by type
- Mean matrix \( M = (m_{ij})^{s}_{i,j} \)
- \( m_{ij} \): expected number of type \( j \) individuals produced by a type \( i \) individual
**Perron-Frobenius theorem**

Let $M$ be positively regular. Then $M$ has a dominant, real-valued, simple eigenvalue $r > 0$, and there exists vectors $\vec{u}, \vec{v}$ with strictly positive coordinates such that

$$M\vec{u} = r\vec{u} \text{ and } \vec{v}'M = r\vec{v}'.$$ 

If $\vec{u}$ and $\vec{v}$ are normalized, so that $\vec{u}'\vec{1} = \vec{v}'\vec{u} = 1$, then

$$\frac{1}{r^k}M^k \rightarrow \vec{u}\vec{v}'$$

as $k \rightarrow \infty$.

- Let the vector $Z_k$ denote the number of realized individuals individuals of generation $k$, then $E(Z_k|Z_0) = (M^k)'Z_0$
- $r$ has the threshold properties of $R_0$
- $r = R_0$
A graph exhibits clustering if it contains a high amount of triangles.
The friends of an individual tends to be friends as well.
Why are short cycles a problem?
- Branching process approximations
Configuration model

1. Start with $N$ nodes
2. Assign a degree (number of half-edges) to each node
3. Match the half-edges uniformly at random
Configuration model with clustering

- Two types of edges: single edges and triangle edges
  1. Start with $N$ nodes
  2. Assign two degrees to each node, a single degree and a triangle degree
  3. Match the half-edges uniformly at random
Miller (2009):

- Disease transmitted along each edge with fixed probability $T$, independently
- Discrete time
- Attributes secondary and tertiary cases in a triangle to primary case.
An SIR model with heterogeneous infectivity

- Underlying social network: configuration graph with clustering
- I.i.d. node weights $\{T_i\}_i$:

$$P(u_i \text{ infects neighbour } u_j \mid T_i) = T_i$$

- Special case: I.i.d. infectious periods, individuals make contact with each neighbour independently at Poisson rate 1
• Sequence \((E_N)_N\) of epidemic processes, where \(N\) denotes the population size

• Construct coupling of \((E_N)_N\) and suitable branching processes:
  - Forward branching processes - ancestor(s) corresponds to initial case(s)
  - Backward branching processes - for each individual \(u\), we explore the individuals that would transmit the disease to \(u\)

• \(u\) contracts the disease if the backward process connects with the forward process

• \(u\) does not contract the disease if the backward process goes extinct
Probability of extinction $\approx$ probability of minor outbreak
Probability of non-extinction \( \approx \) expected fraction infected, given that a major outbreak occurs
$N$: population size

$q$: extinction probability of the approximating forward branching processes

$q_b$: extinction probability of the approximating backward branching processes

$S_N$: the fraction that ultimately escapes infection

**Size of a major outbreak**

\[
S_N \xrightarrow{d} S
\]

as $N \to \infty$ where

\[
S = \begin{cases} 
1 & \text{w.p. } 1 - q \\
q_b & \text{w.p. } q
\end{cases}
\]
The forward process

Type I: Infected along a triangle edge, brother not susceptible
Type II: Infected along a triangle edge, brother susceptible
Type III: Infected along a single edge

Conditioning on the transmission weights and using conditional independence gives $R_0$ and the probability of a major outbreak
Vaccination - forward process

Fraction $f_v$ of population vaccinated with perfect (provides full and permanent immunity) vaccine

Type I: Infected along triangle edge, brother not susceptible
Type II: Infected along triangle edge, brother might be susceptible
Type III: Infected along single edge

$f_v : \text{fraction vaccinated}$

$M_v : \text{mean matrix}$

$M : \text{mean matrix if } f_v = 0$

$M_v = (1 - f_v)M$
Thank you for your attention!
